

## STIC Biotechnology Systems Branch

### CRF Problem Report

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) experienced a problem when processing the following computer readable form (CRF):

Application Serial Number:

10/532,909

Filing Date:

10/13/2005

Date Processed by STIC:

08/22/2006

STIC Contact: Mark Spencer: Telephone: 571-272-2510; Fax: 571-273-0221

#### Nature of CRF Problem:

- ☐ (circle one) Damaged or Unreadable (for Unreadable, see attached)
- ☐ Blank (no files on CRF) (see attached)
- ☐ Empty file (filename present, but no bytes in file) (see attached)
- ☐ Wrong file saved to CRF (invention title, docket number, or applicant(s) do not match those in official application) (see attached)
- ☐ Not saved in ASCII text
- ☐ Sequence Listing was embedded in the file. According to Sequence Rules, submitted file should only be the Sequence Listing.
- ☐ Did not contain a Sequence Listing. (see attached sample)

☒ Other: Invalid Sequence Listing format. Cannot claim a prior application filed before 1st of July - 1998

PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM TO REDUCE ERRORS.  
SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/20/06

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10/33 2, 101 8/22/03

## SEQUENCE LISTING

(1) GENERAL INFORMATION:  
 (iii) NUMBER OF SEQUENCES: 9  
 (2) INFORMATION FOR SEQ ID NO: 1:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 27 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULAR TYPE: DNA  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1  
 AACGgatccaaaacgctgcctccgcga 27

(2) INFORMATION FOR SEQ ID NO: 2:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULAR TYPE: DNA  
 (iv) ANTI-SENSE: YES  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2  
 TAGACGCTGCAGGAGGCGCCTGGCT 25

(2) INFORMATION FOR SEQ ID NO: 3:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 269 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULAR TYPE: DNA  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3  
 ggatccaaaacgctgcctccgcgacagggcggaggacggagggcgctcccaggatcgctggg 60  
 ccttgggcctgacgcctcggagcactccctgctccgagcgggcccgatgtgggtggaagct 120  
 cgggagcgcgggagccgggggaaggccgcggggcagccgctcgggggtccccgatccgagcc 180  
 ccgcggccccgggctggcggtgtcggtgcaatccggcgggcacggccgggcccgggctggg 240  
 ctcttggggcagccaggcgccctccttcag 269

(2) INFORMATION FOR SEQ ID NO: 4:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 84 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULAR TYPE: DNA  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4  
 AGAAGACGAagctaagcagggtcgggcctgggttagtacttggatgggagaccgcctggga 60  
 ataccgggtgctgtaggctttttg 84

(2) INFORMATION FOR SEQ ID NO: 5:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 88 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULAR TYPE: DNA  
 (iv) ANTI-SENSE: YES  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5  
 TCGACAAAAAGCCTACAGCACCCGGTATTCCCAGGCGGTCTCCCATCCAAGTACTAACCA 60  
 GGCCCCACCCTGCTTAGCTTCGTCTTCT 88

(2) INFORMATION FOR SEQ ID NO: 6:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 367 base pairs  
 (B) TYPE: nucleic acid

( Sample of Submitted file )

This is invalid  
 Sequence Listing  
 format. FYI: all  
 US applications which  
 cannot claim a prior  
 application filed before  
 July 1st 1998 must be  
 in New Sequence Rules  
 format. This sequence  
 listing is in  
 old sequence  
 rules format.  
 See sample  
 sequence listing  
 attached for  
 valid format.

# Consult this

<110> Smith, John; Smithgene Inc.

<120> Example of a Sequence Listing

<130> 01-00001

<140> PCT/EP98/00001

<141> 1998-12-31

<150> US 08/999,999

<151> 1997-10-15

<160> 4

<170> PatentIn version 2.0

<210> 1

<211> 389

<212> DNA

<213> Paramecium sp.

<220>

<221> CDS

<222> (279)...(389)

<300>

<301> Doe, Richard

<302> Isolation and Characterization of a Gene Encoding a  
Protease from Paramecium sp.

<303> Journal of Genes

<304> 1

<305> 4

<306> 1-7

<307> 1988-06-31

<308> 123456

<309> 1988-06-31

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tgatgtggca	attgctggca	gtgccacagg	cttttcagcc	aggcttaggg	tgggttccgc		180
cgcggcgcgg	cggcccccct	cgcgctctc	tcgcgcctct	ctctcgctct	cctctcgctc		240

ggacctgatt aggtgagcag gaggaggggg cagtttagc atg gtt tca atg ttc agc 296  
Met Val Ser Met Phe Ser

ttg tct ttc aaa tgg cct gga ttt tgt ttg ttt gtt tgt ttg ttc caa 344  
Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu Phe Val Cys Leu Phe Gln

tgt ccc aaa gtc ctc ccc tgt cac tca tca ctg cag ccg aat ctt 389  
Cys Pro Lys Val Leu Pro Cys His Ser Ser Leu Gln Pro Asn Leu

<210> 2  
<211> 37  
<212> PRT  
<213> Paramecium sp.

<400> 2  
Met Val Ser Met Phe Ser Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu  
1 5 10 15

Phe Val Cys Leu Phe Gln Cys Pro Lys Val Leu Pro Cys His Ser Ser  
20 25 30

Leu Gln Pro Asn Leu  
35

<210> 3  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Designed peptide based on size and polarity to act as a linker between the alpha and beta chains of Protein XYZ.

<400> 3  
Met Val Asn Leu Glu Pro Met His Thr Glu Ile  
1 5 10

<210> 4  
<400> 4  
000

identifiers and their accompanying information as shown in the following table. The numeric identifier shall be used only in the "Sequence Listing." The order and presentation of the items of information in the "Sequence Listing" shall conform to the arrangement given below. Each item of information shall begin on a new line and shall begin with the numeric identifier enclosed in angle brackets as shown. The submission of those items of information designated with an "M" is mandatory. The submission of those items of information designated with an "O" is optional. Numeric identifiers <110> through <170> shall only be set forth at the beginning of the "Sequence Listing." The following table illustrates the numeric identifiers.

Numeric Identifier	Definition	Comments and Format	Mandatory (M) or Optional (O)
<110>	Applicant	Preferably max. of 10 names; one name per line; preferable format: Surname, Other Names and/or Initials	M
<120>	Title of Invention		M
<130>	File Reference	Personal file reference	M when filed prior to assignment of appl. number
<140>	Current Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if available
<141>	Current Filing Date	Specify as: yyyy-mm-dd	M, if available
<150>	Prior Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if applicable include priority documents under 35 USC 119 and 120
<151>	Prior Application Filing Date	Specify as: yyyy-mm-dd	M, if applicable
<160>	Number of SEQ ID NOs	Count includes total number of SEQ ID NOs	M
<170>	Software	Name of software used to create the Sequence Listing	O
<210>	SEQ ID NO:#:	Response shall be an integer representing the SEQ ID NO shown	M
<211>	Length	Respond with an integer expressing the number of bases or amino acid residues	M

<212>	Type	Whether presented sequence molecule is DNA, RNA, or PRT (protein). If a nucleotide sequence contains both DNA and RNA fragments, the type shall be "DNA." In addition, the combined DNA/RNA molecule shall be further described in the <220> to <223> feature section.	M
<213>	Organism	Scientific name, i.e. Genus/species, Unknown or Artificial Sequence... In addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220> to <223> feature section.	M
<220>	Feature	Leave blank after <220>. <221-223> provide for a description of points of biological significance in the sequence.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<221>	Name/Key	Provide appropriate identifier for feature, preferably from WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence
<222>	Location	Specify location within sequence; where appropriate state number of first and last bases/amino acids	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified

in feature

base was used in  
a sequence

<223>

Other Infor-  
mation

Other relevant  
information;  
four lines maximum

M, under the fol-  
lowing conditions:  
if "n," "Xaa," or  
a modified or un-  
usual L-amino acid  
or modified base  
was used in a  
sequence; if  
ORGANISM  
is "Artificial  
Sequence" or  
"Unknown"; if  
molecule is com-  
bined DNA/RNA.

<300>

Publication  
Information

Leave blank  
after <300>

0

<301>

Authors

Preferably max  
of ten named  
authors of publi-  
cation; specify  
one name per line;  
preferable format:  
Surname, Other  
Names and/or  
Initials

0

<302>

Title

0

<303>

Journal

0

<304>

Volume

0

<305>

Issue

0

<306>

Pages

0

<307>

Date

Journal date on which  
data published;  
specify as yyyy-mm-  
dd, MM-yyyy or  
Season-yyyy

0

<308>

Database  
Accession  
Number

Accession number  
assigned by data-  
base including  
database name

0

<309>

Database Entry  
Date

Date of entry in  
database; specify  
as yyyy-mm-dd or  
MM-yyyy

0

<310>

Patent Document  
Number

Document number;  
for patent-type  
citations only.  
Specify as, for  
example, US  
07/999,999

0

3

<311>	Patent Filing Date	Document filing date, for patent-type citations only; specify as yyyy-mm-dd	O
<312>	Publication Date	Document publication date, for patent-type citations only; specify as yyyy-mm-dd	O
<313>	Relevant Residues	FROM (position) TO (position)	O
<400>	Sequence	SEQ ID NO should follow the numeric identifier and should appear on the line preceding the actual sequence	M

5. Section 1.824 is revised to read as follows:

1.824 Form and format for nucleotide and/or amino acid sequence submissions in computer readable form.

(a) The computer readable form required by 1.821(e) shall meet the following specifications:

(1) The computer readable form shall contain a single "Sequence Listing" as either a diskette, series of diskettes, or other permissible media outlined in paragraph (c) of this section.

(2) The "Sequence Listing" in paragraph (a) (1) of this section shall be submitted in American Standard Code for Information Interchange (ASCII) text. No other formats shall be allowed.

(3) The computer readable form may be created by any means, such as word processors, nucleotide/amino acid sequence editors or other custom computer programs; however, it shall conform to all specifications detailed in this section.

(4) File compression is acceptable when using diskette media, so long as the compressed file is in a self-extracting format that will decompress on one of the systems described in paragraph (b) of this section.

(5) Page numbering shall not appear within the computer readable form version of the "Sequence Listing" file.

(6) All computer readable forms shall have a label permanently affixed thereto on which has been hand-printed or typed: the name of the applicant, the title of the invention, the date on which the data were recorded on the computer readable form, the operating system used, a reference number, and an application serial number and filing date, if known.

(b) Computer readable form submissions must meet these format requirements:

(1) Computer: IBM PC/XT/AT, or compatibles, or Apple Macintosh;

(2) Operating System: MS-DOS, Unix or Macintosh;



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